

SEQUENCE LISTING

<110> Colyer, John  
Bhogal, Moninder Singh

<120> METHOD AND PRODUCTS FOR THE SELECTIVE DEGRADATION OF PROTEINS

<130> 9052-249

<150> PCT/GB2005/000811  
<151> 2005-03-03

<150> GB0404731.2  
<151> 2004-03-03

<160> 12

<170> PatentIn version 3.3

<210> 1  
<211> 6  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (4)..(5)  
<223> Xaa can be any naturally occurring amino acid

<400> 1

Asp Ser Gly Xaa Xaa Ser  
1 5

<210> 2  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> oligonucleotide primer

<400> 2  
cgggatccat ggataaagtc catacc 26

<210> 3  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> oligonuceotide primer

<400> 3  
cccaagcttt tagagaagca tcaaattg 27

<210> 4

<211> 27  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 4  
 gcgggatcca tggataaagt ccatacc 27

<210> 5  
 <211> 27  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 5  
 cccaagcttt tagagaagca tcaaattg 27

<210> 6  
 <211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 6  
 cctttgatat tggatcctaa gcttttagag 30

<210> 7  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 7  
 cggtggggga ggcggtgggg gaggcggatc catggataga gtcca 45

<210> 8  
 <211> 36  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 8  
 catctctaga acctgcaggg aatgcagatc ttcgtg 36

<210> 9  
 <211> 45

<212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 9  
 ccccaccgcc tccccaccg cctccctcga gacggccgcc cctca 45

<210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 10  
 gggccgctct aaaacccgca ggga 24

<210> 11  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> oligonucleotide primer  
  
 <400> 11  
 aagcctctag agaagcatca caat 24

<210> 12  
 <211> 1349  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 12

Glu Thr Leu Asp Glu Gly Met Gln Ile Pro Ser Thr Gln Phe Asp Ala  
 1 5 10 15

Ala His Pro Thr Asn Val Gln Arg Leu Ala Glu Pro Ser Gln Met Leu  
 20 25 30

Lys His Ala Val Val Asn Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu  
 35 40 45

Ala Thr Arg Ala Ile Pro Glu Leu Thr Lys Leu Leu Asn Asp Glu Asp  
 50 55 60

Gln Val Val Val Asn Lys Ala Ala Val Met Val His Gln Leu Ser Lys  
 65 70 75 80

Lys Glu Ala Ser Arg His Ala Ile Met Arg Ser Pro Gln Met Val Ser  
 85 90 95

Ala Ile Val Arg Thr Met Gln Asn Thr Asn Asp Val Glu Thr Ala Arg  
 100 105 110

Cys Thr Ala Gly Thr Leu His Asn Leu Ser His His Arg Glu Gly Leu  
 115 120 125

Leu Ala Ile Phe Lys Ser Gly Gly Ile Pro Ala Leu Val Lys Met Leu  
 130 135 140

Gly Ser Pro Val Asp Ser Val Leu Phe Tyr Ala Ile Thr Thr Leu His  
 145 150 155 160

Asn Leu Leu Leu His Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala  
 165 170 175

Gly Gly Leu Gln Lys Met Val Ala Leu Leu Asn Lys Thr Asn Val Lys  
 180 185 190

Phe Leu Ala Ile Thr Thr Asp Cys Leu Gln Ile Leu Ala Tyr Gly Asn  
 195 200 205

Gln Glu Ser Lys Leu Ile Ile Leu Ala Ser Gly Gly Pro Gln Ala Leu  
 210 215 220

Val Asn Ile Met Arg Thr Tyr Thr Tyr Glu Lys Leu Leu Trp Thr Thr  
 225 230 235 240

Ser Arg Val Leu Lys Val Leu Ser Val Cys Ser Ser Asn Lys Pro Ala  
 245 250 255

Ile Val Glu Ala Gly Gly Met Gln Ala Leu Gly Leu His Leu Thr Asp  
 260 265 270

Pro Ser Gln Arg Leu Val Gln Asn Cys Leu Trp Thr Leu Arg Asn Leu  
 275 280 285

Ser Asp Ala Ala Thr Lys Gln Glu Gly Met Glu Gly Leu Leu Gly Thr  
 290 295 300

Leu Val Gln Leu Leu Gly Ser Asp Asp Ile Asn Val Val Thr Cys Ala  
 305 310 315 320

Ala Gly Ile Leu Ser Asn Leu Thr Cys Asn Asn Tyr Lys Asn Lys Met

325					330					335					
Met	Val	Cys	Gln	Val	Gly	Gly	Ile	Glu	Ala	Leu	Val	Arg	Thr	Val	Leu
			340					345					350		
Arg	Ala	Gly	Asp	Arg	Glu	Asp	Ile	Thr	Glu	Pro	Ala	Ile	Cys	Ala	Leu
		355					360					365			
Arg	His	Leu	Thr	Ser	Arg	His	Gln	Glu	Ala	Glu	Met	Ala	Gln	Asn	Ala
	370					375					380				
Val	Arg	Leu	His	Tyr	Gly	Leu	Pro	Val	Val	Val	Lys	Leu	Leu	His	Pro
385					390					395					400
Pro	Ser	His	Trp	Pro	Leu	Ile	Lys	Ala	Thr	Val	Gly	Leu	Ile	Arg	Asn
				405					410					415	
Leu	Ala	Leu	Cys	Pro	Ala	Asn	His	Ala	Pro	Leu	Arg	Glu	Gln	Gly	Ala
			420					425					430		
Ile	Pro	Arg	Leu	Val	Gln	Leu	Leu	Val	Arg	Ala	His	Gln	Asp	Thr	Gln
		435					440					445			
Arg	Arg	Thr	Ser	Met	Gly	Gly	Thr	Gln	Gln	Gln	Phe	Val	Glu	Gly	Val
	450					455					460				
Arg	Met	Glu	Glu	Ile	Val	Glu	Gly	Cys	Thr	Gly	Ala	Leu	His	Ile	Leu
465					470					475					480
Ala	Arg	Asp	Val	His	Asn	Arg	Ile	Val	Ile	Arg	Gly	Leu	Asn	Thr	Ile
				485					490					495	
Pro	Leu	Phe	Val	Gln	Leu	Leu	Tyr	Ser	Pro	Ile	Glu	Asn	Ile	Gln	Arg
			500					505					510		
Val	Ala	Ala	Gly	Val	Leu	Cys	Glu	Leu	Ala	Gln	Asp	Lys	Glu	Ala	Ala
		515					520					525			
Glu	Ala	Ile	Glu	Ala	Glu	Gly	Ala	Thr	Ala	Pro	Leu	Thr	Glu	Leu	Leu
	530					535					540				
His	Ser	Arg	Asn	Glu	Gly	Val	Ala	Thr	Tyr	Ala	Ala	Ala	Val	Leu	Phe
545					550					555					560
Arg	Met	Ser	Glu	Asp	Lys	Pro	Gln	Asp	Tyr	Lys	Lys	Arg	Leu	Ser	Val
				565					570					575	

Glu Leu Thr Ser Ser Leu Phe Arg Thr Glu Pro Met Ala Trp Asn Glu  
580 585 590

Thr Ala Asp Leu Gly Leu Asp Ile Gly Ala Gln Gly Glu Ala Leu Gly  
595 600 605

Tyr Arg Gln Asp Asp Pro Ser Tyr Arg Ser Phe His Ser Gly Gly Tyr  
610 615 620

Gly Gln Asp Ala Leu Gly Met Asp Pro Met Met Glu His Glu Met Gly  
625 630 635 640

Gly His His Pro Gly Ala Asp Tyr Pro Val Asp Gly Leu Pro Asp Leu  
645 650 655

Gly His Ala Gln Asp Leu Met Asp Gly Leu Pro Pro Gly Asp Ser Asn  
660 665 670

Gln Leu Ala Trp Phe Asp Thr Asp Leu Gly Ser Asn Met Asp Pro Ala  
675 680 685

Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met Asn Ser Ser Glu  
690 695 700

Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys Ile Ile Pro Glu  
705 710 715 720

Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala Arg Leu Cys Ile  
725 730 735

Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met Lys Thr Glu Asn  
740 745 750

Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser Ser Met Ile Val  
755 760 765

Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys Glu Lys Glu Leu  
770 775 780

Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp Gln Val Glu Phe  
785 790 795 800

Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln His Gly His Ile  
805 810 815

Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala Leu  
820 825 830

Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu  
835 840 845

Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp Tyr  
850 855 860

Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Met  
865 870 875 880

Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp  
885 890 895

Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu Asn Ala Pro Pro  
900 905 910

Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu  
915 920 925

Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg Ile  
930 935 940

His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr Asp  
945 950 955 960

Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile Trp  
965 970 975

Asp Lys Ser Thr Leu Glu Cys Lys Arg Ile Leu Thr Gly His Thr Gly  
980 985 990

Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly Ser  
995 1000 1005

Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Ala Gly Glu Met  
1010 1015 1020

Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His Leu Arg  
1025 1030 1035

Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile  
1040 1045 1050





1280		1285		1290
Pro Tyr Asp Ser Leu Leu Val Phe Asp Tyr Glu Gly Ser Gly Ser				
1295		1300		1305
Glu Ala Ala Ser Leu Ser Ser Leu Asn Ser Ser Glu Ser Asp Gln				
1310		1315		1320
Asp Gln Asp Tyr Asp Tyr Leu Asn Glu Trp Gly Asn Arg Phe Lys				
1325		1330		1335
Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp				
1340		1345		